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First record of the *Heterotoma planicornis* (Hemiptera, Heteroptera, Miridae), an introduced species in the Korean Peninsula, with characterization of its complete mitochondrial genome

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Abstract

The West Palearctic genus *Heterotoma* Lepeletier & Serville, 1825, and its included species *H. planicornis* (Pallas, 1772) (Hemiptera, Heteroptera, Miridae, Orthotylinae) are reported from the Korean Peninsula. *Heterotoma planicornis* is diagnosed, and its dorsal habitus and the genitalia of both sexes are illustrated. The possible introduction of this European species into the Korean Peninsula is discussed. The complete mitochondrial genome of the species is provided. The circular mitogenome of *H. planicornis* is 16,179 bp long, comprising 13 protein-coding genes, two ribosomal RNA genes, and 22 transfer RNAs, and shows the same gene order as the closely allied species *Mecomma ambulans* (Fallén, 1807). The A–T content of the total sequence was 71.54%. An analysis using a cytochrome oxidase I (COI) neighbor-joining (NJ) tree revealed that the Korean *H. planicornis* population formed two distinctive groups, with a 1.8% sequence difference between them.

Key Words

species introduction, distribution, East Asia, mitogenome, phylogeny, plant bugs

Introduction

Orthotylinae is a subfamily of Miridae (Hemiptera: Heteroptera), comprising approximately six tribes, 260 genera, and over 2,100 described species (Schuh 2002–2013; Schuh and Weirauch 2020; Oh et al. 2023). A morphology-based analysis recovered this subfamily as a close relative of Phylinae (Schuh 1976), and this was further supported by subsequent molecular-based phylogenetic analyses (Menard et al. 2014; Oh et al. 2023). Orthotyline species are predominantly predators, and some of them are natural enemies of pests of various plants (Wheeler 2001; Oh et al. 2023). *Heterotoma* species are zoophytophagous and recognized as natural enemies of various pest arthropods; *H. planicornis* has been reported to prey on mites, aphids, psyllids, gall midges, eggs and larvae of Chrysomelidae, as well as eggs of heteropteran and lepidopteran insects (for review, see Kment and Bryja 2006).

Currently, four *Heterotoma* species are known, all native to the Western Palearctic (Wheeler and Henry 1992; Kerzhner and Josifov 1999; Schuh 2002–2013). Among them, *H. planicornis* exhibits the widest distribution; in addition to its native Western Palearctic area, it has been introduced to North America (Canada, USA) (Knight 1917; Wheeler and Henry 1992). An observation from the Republic of South Africa (Western Cape) has been reported by iNaturalist (2025), but the correct identification of this record requires verification.

In this paper, we present a new distribution record of *Heterotoma planicornis* from the Korean Peninsula. A morphological diagnosis is presented, and the habitus of the species and genitalia of both sexes are illustrated. The

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complete mitogenome sequence of *H. planicornis* is provided and compared to those of related taxa by a neighbor-joining (NJ) tree based on the cytochrome oxidase I (COI) region.

Materials and methods

Specimen examination and figure acquisition

All voucher specimens are deposited in the collection of the Insect Biosystematics Laboratory, Research Institute for Agriculture and Life Science, Seoul National University, Korea (SNU). Digital images of external characteristics were taken with a DMC 5400 digital camera attached to a Leica Z16 APO motorized microscope. Genital structures were dissected and observed under a Leica DM 4000B microscope, and images were taken using a digital camera combined with the microscope (Lumenera Infinity 3). All measurements (mean and range) are provided in millimeters. Terminology for male and female genital structures follows Oh and Lee (2018).

Mitogenome data construction

Genomic DNA was extracted from the abdominal segments IV–VI and legs of specimens preserved in 95% to 99% alcohol using a DNeasy Blood and Tissue Kit (QIAGEN, Inc.) following the manufacturer's protocols. Examined specimens were labeled and stored in alcohol depending on their condition. After DNA extraction, a sequencing library was prepared using the TruSeq Nano DNA Kit, based on the TruSeq Nano DNA Sample Preparation Guide, Part #15041110 Rev. D (Illumina, Inc.). NovaSeq X Plus was used as the sequencing platform. Read length was 151 bp (30 million reads per lane) according to the Macrogen Company (South Korea) sequencing facility. Sequences were aligned using Geneious Prime 2025.1.3 software (Kearse et al. 2012). A total of six reference sequences were used for alignment (Table 1), and the resulting data were annotated using MITOS2 (Bernt et al. 2013) and visualized as a circular map using the webserver Proksee (https://proksee.ca/, accessed on 26 July 2024) (Grant et al. 2023).

Phylogenetic analysis

A COI-based dataset, comprising 10 sequences from the NCBI database and four from the present study, was compiled. To evaluate inter- and intraspecific genetic distances, 563 bp of the mitochondrial protein-coding COI (cytochrome oxidase subunit I) gene was used (Folmer et al. 1994), with LCO1490 (5′-GGTCAACAAATCATAAAGATATTGG-3′) and HCO2198 (5′-TAAACTTCAGGGTGACCAAAAAATCA-3′) primers. During alignment, an L-INS-i strategy was used, without any manipulation except trimming the ends of reads. A neighbor-joining (NJ) tree (Saitou and Nei 1987) was generated, and sequence divergences were evaluated using the Kimura 2-parameter model (K2P) (Kimura 1980) in MEGA 7.0 (Kumar et al. 2016). Detailed information for the sequences used is provided in Table 2.

Table 1. Sequences used for the annotation of the mitochondrial genome of *Heterotoma planicornis*.

Subfamily	Tribe	Species	Accession No.	Locality	bp	Reference
Mirinae	Hyalopeplini	*Onomaus tenuis* Zheng, 2004	MW619699.1	Unknown	14860	Ye et al. (2022)
Mirinae	Mecistoscelini	*Mystilus priamus* Distant, 1904	MW619697.1	Unknown	14687	Ye et al. (2022)
Mirinae	Mirini	*Adelphocoris suturalis* (Jakovlev, 1882)	KJ020288.1	China	14327	Wang et al. (2014)
Mirinae	Stenodemini	*Trigonotylus caelestialium* (Kirkaldy, 1902)	KJ170899.1	China	15095	Wang et al. (2014)
Orthotylinae	Orthotylini	*Mecomma ambulans* (Fallén, 1807)	MW619692.1	Unknown	12613	Ye et al. (2022)
Phylinae	Pilophorini	*Pilophorus typicus* (Distant, 1909)	MW619694.1	Unknown	15335	Ye et al. (2022)

Table 2. COI sequences used for phylogenetic analysis in this study.

Subfamily	Tribe	Species	Accession No.	Locality	bp	Reference
Orthotylinae	Halticini	*Ectmetopterus comitans* (Josifov & Kerzhner, 1972)	GU194790.1	Unknown	527	Jung and Lee (2012)
Orthotylinae	Halticini	*Orthocephalus funestus* Jakovlev, 1881	GU194802.1	Unknown	527	Jung and Lee (2012)
Orthotylinae	Halticini	*Strongylocoris leucocephalus* (Linnaeus, 1758)	KM022178.1	Germany	658	Raupach et al. (2014)
Orthotylinae	Orthotylini	*Blepharidopterus diaphanus* (Kirschbaum, 1856)	MZ407988	Korea	563	Oh et al. (2023)
Orthotylinae	Orthotylini	*Dryophilocoris miyamotoi* Yasunaga, 1999	GU194785.1	Unknown	527	Jung and Lee (2012)
Orthotylinae	Orthotylini	*Heterotoma planicornis* (Pallas, 1772)	HQ105735.1	Canada	638	Park et al. (2011)
Orthotylinae	Orthotylini	*Heterotoma planicornis* (Pallas, 1772)	HQ105736.1	Canada	638	Park et al. (2011)
Orthotylinae	Orthotylini	*Heterotoma planicornis* (Pallas, 1772)	PV879916	Korea	16179	This work
Orthotylinae	Orthotylini	*Heterotoma planicornis* (Pallas, 1772)	PV789749	Korea	563	This work
Orthotylinae	Orthotylini	*Heterotoma planicornis* (Pallas, 1772)	PV850443	Korea	563	This work
Orthotylinae	Orthotylini	*Heterotoma planicornis* (Pallas, 1772)	PV850444	Korea	563	This work
Orthotylinae	Orthotylini	*Orthotylus pallens* (Matsumura, 1911)	GU194805.1	Unknown	527	Jung and Lee (2012)
Orthotylinae	Orthotylini	*Ulmica yasunagai* Oh & Lee, 2018	MZ408099	Korea	563	Oh et al. (2023)
Orthotylinae	Orthotylini	*Zanchius tarasovi* Kerzhner, 1988	MZ408103	Korea	563	Oh et al. (2023)

Taxonomy

Genus *Heterotoma* Lepeletier & Serville, 1825

Pachycera Billberg, 1820: 68 (original description). Type species: *Cimex spissicornis* Fabricius, 1777 (= *Cimex planicornis* Pallas, 1772), by monotypy. *Nomen oblitum*. Synonymized by Kerzhner (1997: 245).

Heterotoma Lepeletier & Serville, 1825: 326 (original description). Type species: *Cimex planicornis* Pallas, 1772, by monotypy.

Acroderrhis Bergroth, 1914: 179 (original description). Type species: *Heterotoma dentipennis* Bergroth, 1914, by monotypy. Synonymized by Wagner (1968: 182).

Heterotoma: Schuh (1995: 120) (catalog); Kerzhner and Josifov (1999: 248) (catalog); Schuh (2002–2013) (online catalog); Kment and Bryja (2006: 11) (diagnosis); Aukema (2018) (online catalog).

Heterotoma planicornis (Pallas, 1772)

Figs 1–6

Cimex planicornis Pallas, 1772: 23. (original description).

Cimex spissicornis Fabricius, 1777: 300 (original description). Synonymized by Costa (1843: 55).

Acanthia crassicornis Fabricius, 1794: 70 (original description). Synonymized by Reuter (1888: 667).

Cimex crassipennis Turton, 1802: 609 (new name for *Cimex crassicornis*). Synonymized by Reuter (1888: 667).

Heterotoma acinaciformis Costa, 1839: 20 (original description). Synonymized by Wagner (1968: 185), tentatively.

Heterotoma planicornis: Tamanini (1962: 136) (diagnosis, description); Schuh (1995: 121) (catalog); Kerzhner and Josifov (1999: 248) (catalog); Schuh (2002–2013) (online catalog); Kment and Bryja (2006: 11) (redescription, figures, neotype designation, distribution, biol-

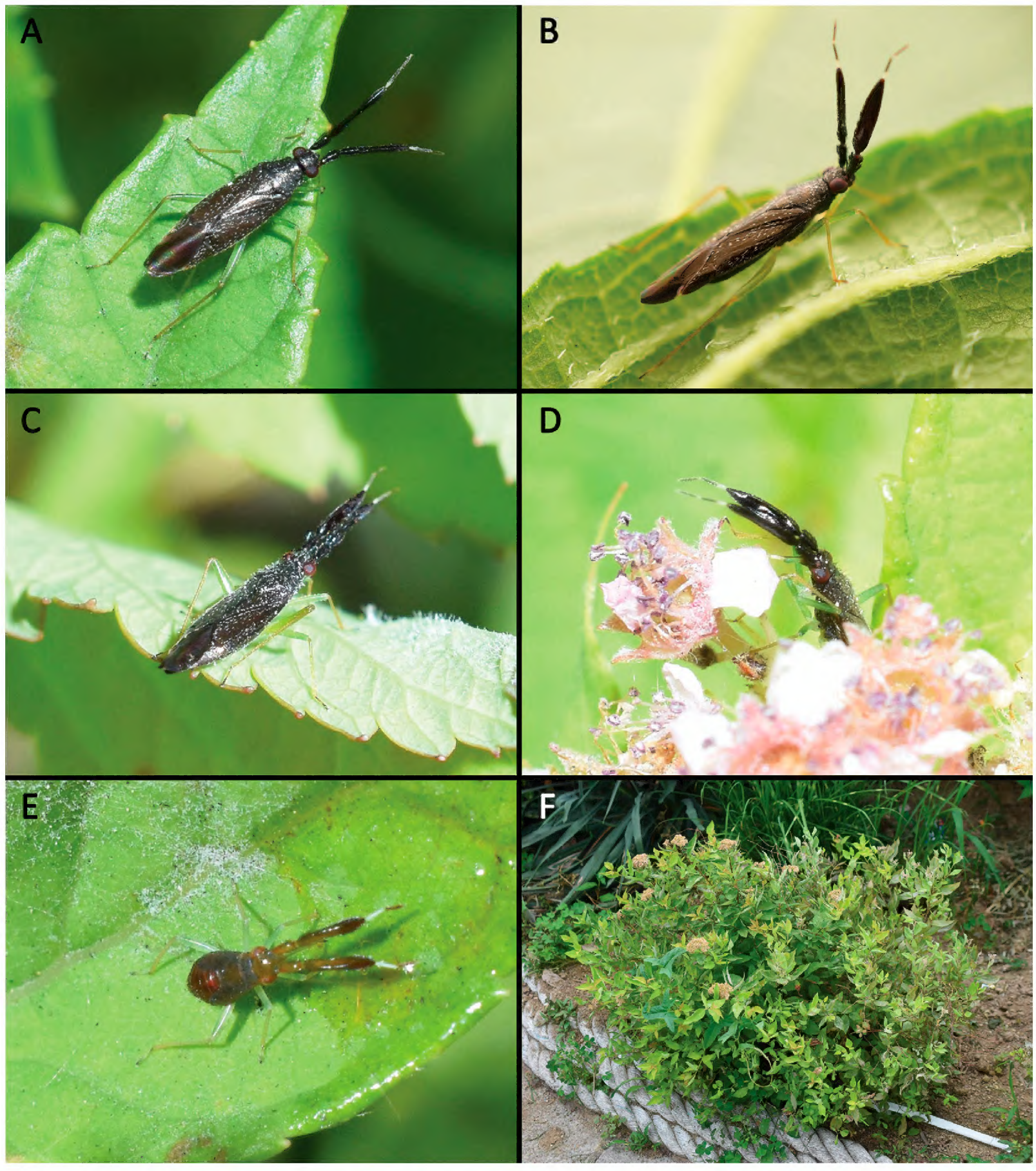

Figure 1. *Heterotoma planicornis*, live individuals. **A, B, D.** Male; **C.** Female; **E.** Last instar nymph; **F.** Collection site, with host plant *Spiraea japonica* 'Goldflame'.

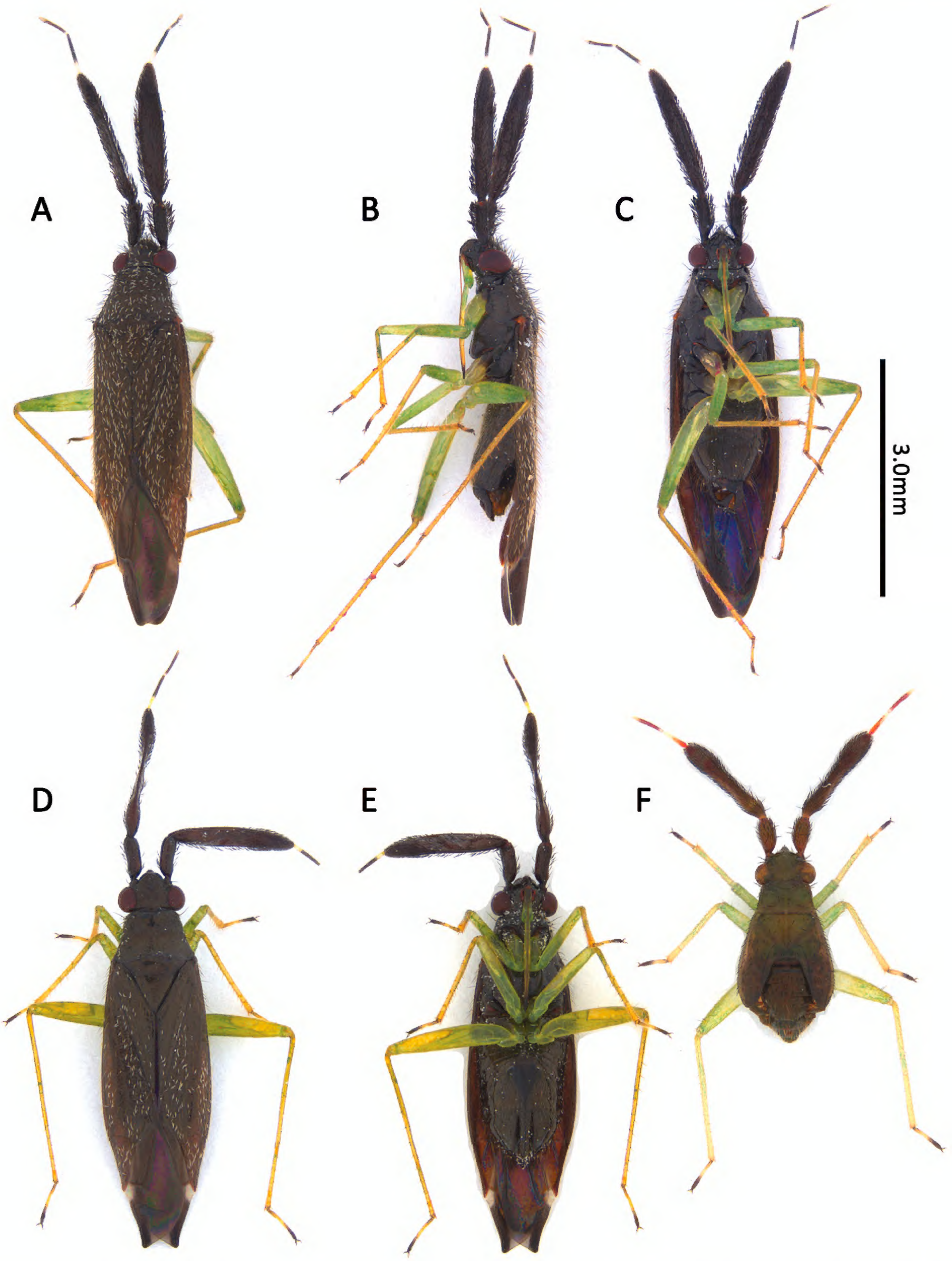

Figure 2. Dorsal and ventral habitus of Korean *Heterotoma planicornis*. **A–C.** Male; **D, E.** Female; **F.** Last instar nymph. Scale bar: 3.0 mm.

ogy); Kment and Bryja (2012: 117) (correction); Aukema (2018) (online catalog).

Diagnosis. This species can be distinguished by the combination of the following characters: dorsum covered with brown, suberect setae and pale, reclining sericeous setae (Figs 1A–E, 2A, D); antennal segment blackish brown, segments I and II densely covered with fuscous, suberect setae; segment II thick and elongated, somewhat flattened (Figs 1A–E, 2A–F); segments

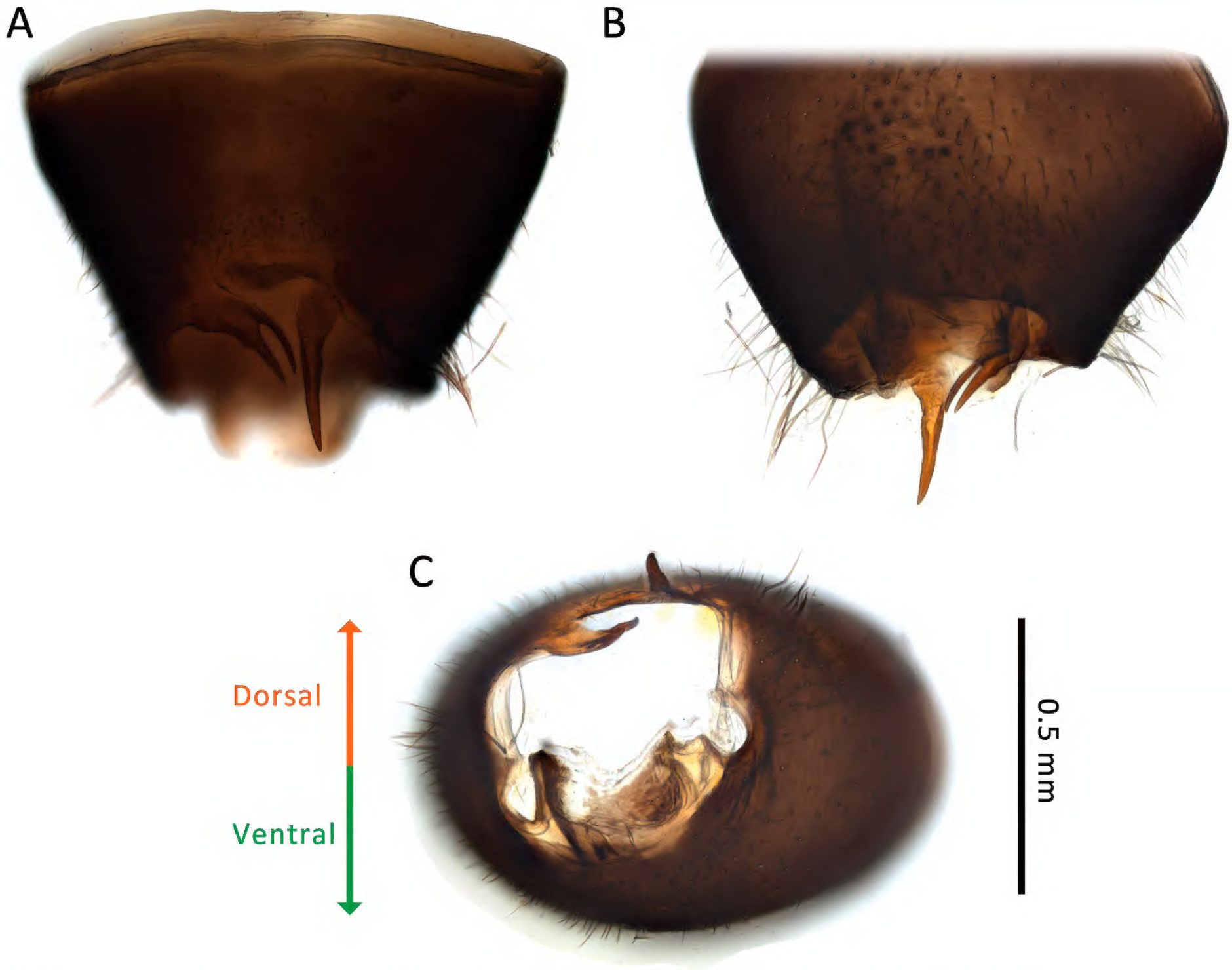

Figure 3. Pygophore of *Heterotoma planicornis*. **A.** Dorsal view; **B.** Ventral view; **C.** Pygophore opening. Scale bar: 0.5 mm.

III and IV short, thin, and linear, basally pale; hemelytra entirely dark brown; labium reaching mesocoxae; femora pale green, without dark or reddish tinge; tibiae yellowish green, subbasally tinged with green; tarsus yellowish green, widely darkened at segments I and III; pygophore with one elongated, pointed-end structure and short, bifurcate structure (Fig. 3A–C); male endosoma with two elongated, apically spinulate sclerites and thick and smooth, pointed-end basal sclerite (Fig. 4A–D); sensory lobe of left paramere with thick structure covered with stiff setae, hypophysis with minute, hook-like structure (Fig. 4E–G); sensory lobe of right paramere moderately curved and laterally with two dentation, hypophysis stout, apically blunt (Fig. 4H–J); female genitalia with thick sclerotized ring (Fig. 5A–C); interramal lobe spinulate, bifurcate proximally (Fig. 5D, E). For more diagnostic characters and figures, see Tamanini (1962, 1981) and Kment and Bryja (2006, 2012).

Measurements. ***Male*** (n = 5) / ***Female*** (n = 2). Total body length 4.45–5.00 / 4.75–4.85; head width across eyes 0.79–0.84 / 0.83–0.85; vertex width 0.33–0.36 / 0.35–0.39; lengths of antennal segments I–IV 0.53–0.59, 1.66–1.79, 0.49–0.53, 0.42–0.47 / 0.54–0.55, 1.64–1.70, 0.49–0.50, 0.44; labial length 1.57–1.63 / 1.53–1.65; mesal pronotal length including collar 0.63–0.71 / 0.61–0.62; basal pronotal width 1.01–1.12 / 1.04–1.10; width across hemelytron 1.28–1.39 / 1.39–1.63; cuneal length 0.69–0.88 / 0.76–0.78; cuneal width 0.33–0.39 / 0.33–0.35; lengths of metafemur, tibia, and tarsus 1.49–1.66, 2.05–2.40, 0.47–0.55 / 1.56–1.65, 2.13–2.22, 0.53–0.54.

Distribution. Europe: most of the territory. **Asia:** Türkiye, South Korea (introduced) (**new record**). **North America**: Canada, USA (Wheeler and Henry 1992; Kerzhner and Josifov 1999; Kment and Bryja 2006) (introduced).

Biology. This species exhibits a wide host range, feeding on plants from 12 angiosperm families (Kment and Bryja 2006). Our observations revealed that the Korean population inhabits *Spiraea japonica* (Rosaceae) (Fig. 1F). The habitat of *H. planicornis* discovered in this study was limited to narrow artificial landscapes in urbanized areas, excluding larger available natural habitats such as parks.

Material examined. South Korea, Seoul: 5♂, 1♀, near Hannam station, Dokseodang-ro 6, Yongsan-gu, on *Spiraea japonica* 3.vi.2024, Soojeong Cho (SNU); 1♀, ditto, 17.vi.2023, Soojeong Cho (SNU); 1♂, ditto, 5.vi.2024, Minsuk Oh (NIBR).

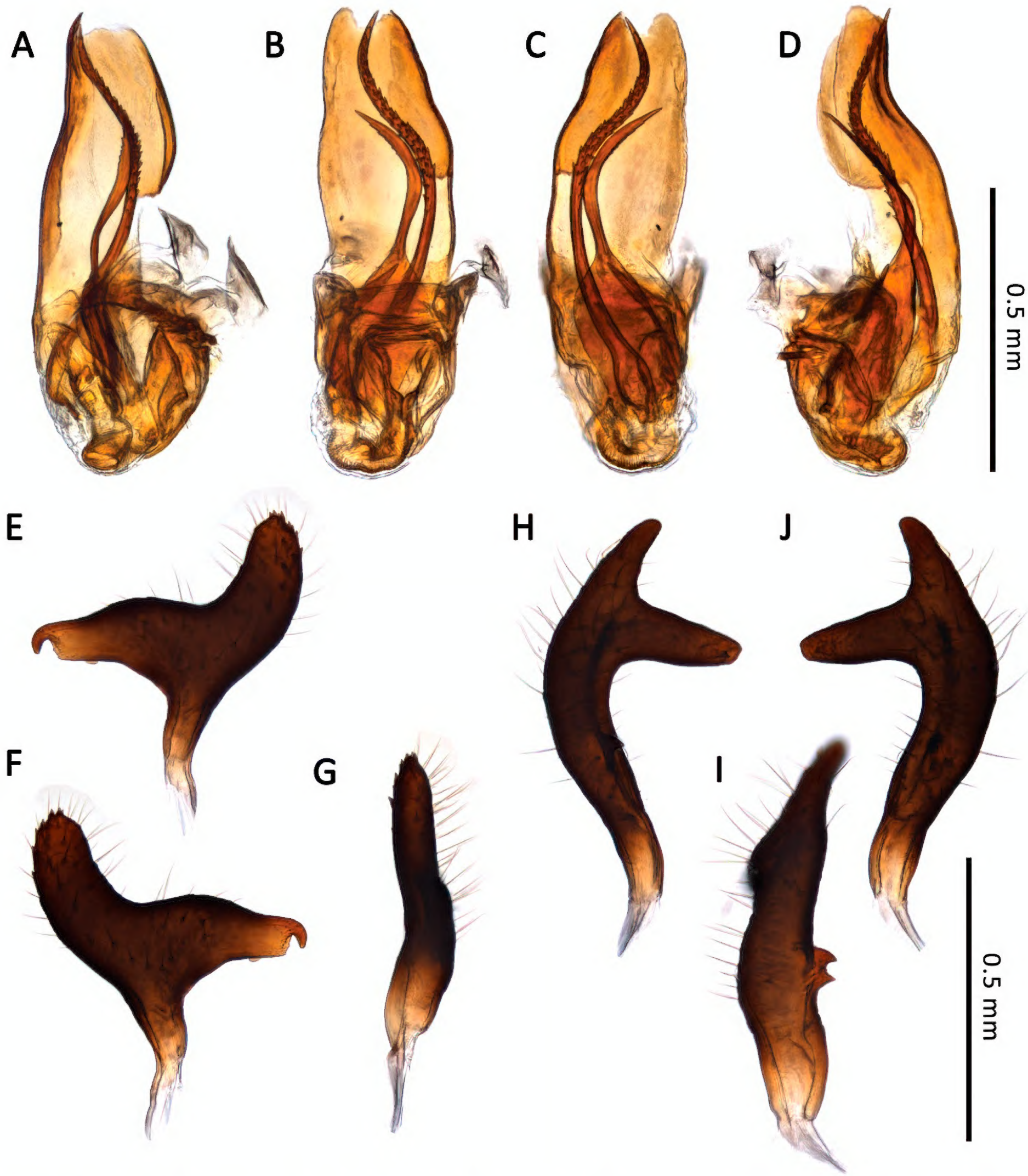

Figure 4. Male genitalia of *Heterotoma planicornis*. **A–D.** Endosoma; **E–G.** Left paramere; **H–J.** Right paramere. Scale bars: 0.5 mm.

Result

In this study, the mitogenome sequence of *H. planicornis* is documented for the first time (Fig. 6). Its full length is 16,179 bp, comprising 13 protein-coding genes (PCGs), two rRNA genes, 22 tRNA genes, and a control region. The gene composition is similar to that of other previously sequenced mitochondrial genomes of Miridae (Wang et al. 2014). The average GC content of the full sequence was 28.46%. Among PCGs, GC content was the lowest at ATP synthase subunit 8 (*atp8*, 22.01%) and the highest at cytochrome oxidase subunit I (COI, 36.39%). Unlike other mirid genome sequences, the mitogenome of *H. planicornis* did not have a positive GC skew except in the control region. Additional information about each gene sequence is provided in Table 3.

In the NJ tree and pairwise distance analysis using COI sequences (Fig. 7, Table 4), the sequence extracted from the mitogenome of a male *H. planicornis* (PV879916) and one female (PV850444) showed a 1.90–1.98% genetic distance compared to the Canadian population (HQ105735.1, HQ105736.1), whereas sequences from a last instar nymph (PV850443) and a male (PV789749) were almost identical.

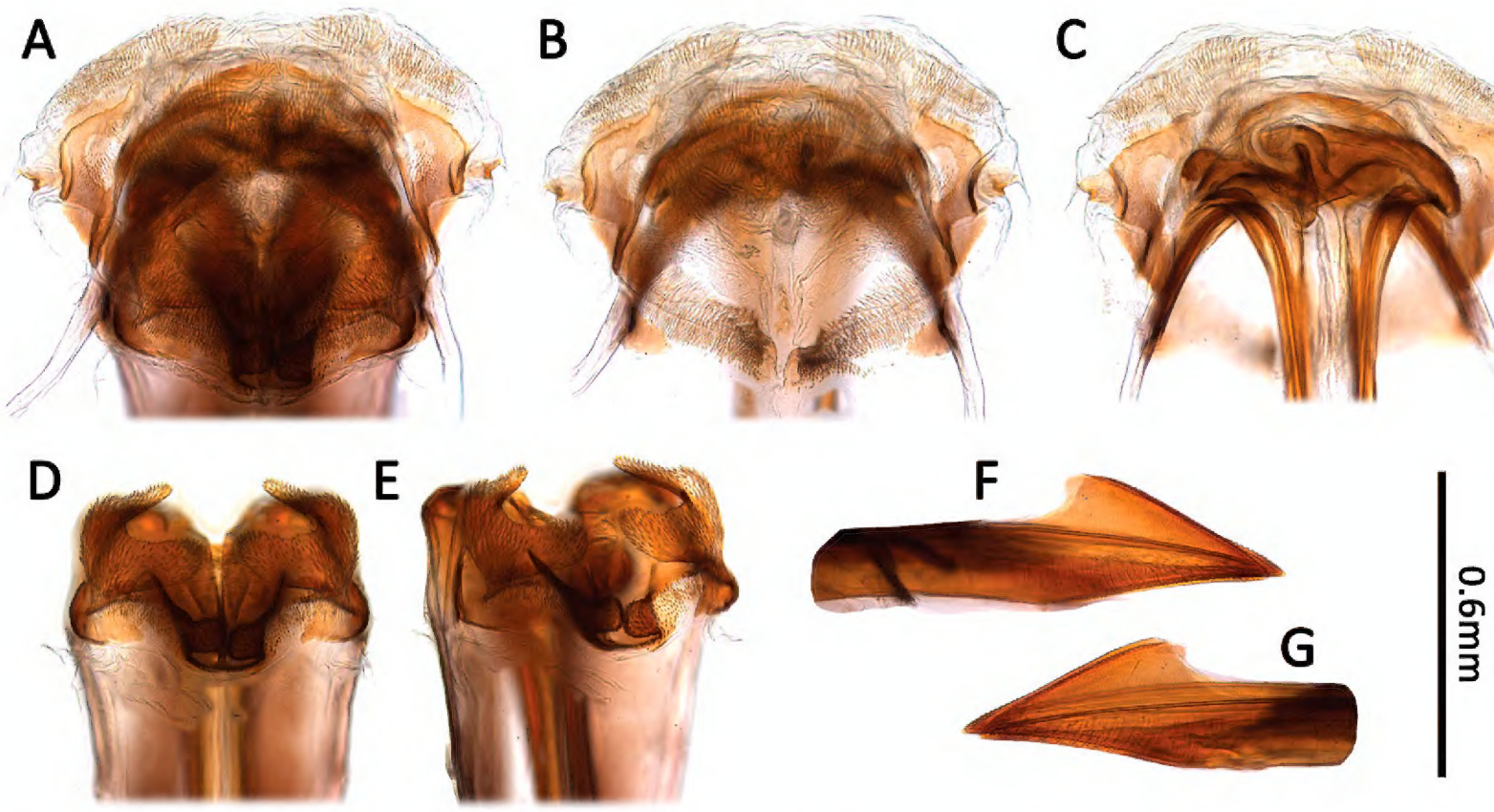

Figure 5. Female genitalia of *Heterotoma planicornis*. **A.** Bursa copulatrix (before dissecting posterior wall); **B.** Bursa copulatrix, dorsal view; **C.** Bursa copulatrix, ventral view; **D, E.** Posterior wall; **F, G.** Gonapophysis II. Scale bar: 0.6 mm.

Table 3. Gene composition of the mitochondrial genome of *Heterotoma planicornis*. Sequences were annotated by MITOS2, powered by the Proksee webserver. GC contents of each gene were calculated using the VectorBuilder GC Content Calculator (Cyagen Biosciences Inc. 2024).

Type	Name	Start	Stop	Strand	GC contents (%)	Anti-codon
tRNA	trnI (tRNA-Isoleucine)	1	66	1	21.21	GAT
tRNA	trnQ (tRNA-Glutamine)	64	132	-1	24.64	TTG
tRNA	trnM (tRNA-Methionine)	132	200	1	24.64	CAT
PCG	nad2 (NADH dehydrogenase subunits II)	258	1202	1	27.2	-
tRNA	trnW (tRNA-Tryptophan)	1201	1264	1	15.63	TCA
tRNA	trnC (tRNA-Cysteine)	1257	1319	-1	26.98	GCA
tRNA	trnY (tRNA-Tyrosine)	1319	1382	-1	26.56	GTA
PCG	cox1 (cytochrome oxidase subunits I)	1383	2921	1	36.39	-
tRNA	trnL2 (tRNA-Leucine2)	2917	2981	1	26.15	TAA
PCG	cox2 (cytochrome oxidase subunits II)	2983	3664	1	32.84	-
tRNA	trnK (tRNA-Lysine)	3662	3731	1	31.43	CTT
tRNA	trnD (tRNA-Aspartic Acid)	3731	3795	1	10.77	GTC
PCG	atp8 (ATP synthase subunits 8)	3796	3954	1	22.01	-
PCG	atp6 (ATP synthase subunits 6)	3948	4619	1	31.99	-
PCG	cox3 (cytochrome oxidase subunits III)	4619	5405	1	33.29	-
tRNA	trnG (tRNA-Glycine)	5403	5464	1	20.97	TCC
PCG	nad3 (NADH dehydrogenase subunits III)	5480	5830	1	29.34	-
tRNA	trnA (tRNA-Alanine)	5817	5878	1	25.81	TGC
tRNA	trnR (tRNA-Arginine)	5883	5946	1	34.38	TCG
tRNA	trnN (tRNA-Asparagine)	5946	6012	1	22.39	GTT
tRNA	trnS1 (tRNA-Serine1)	6012	6080	1	33.33	GCT
tRNA	trnE (tRNA-Glutamic Acid)	6080	6143	1	21.88	TTC
tRNA	trnF (tRNA-Phenylalanine)	6142	6205	-1	26.56	GAA
PCG	nad5 (NADH dehydrogenase subunits V)	6186	7898	-1	25.51	-
tRNA	trnH (tRNA-Histidine)	7899	7962	-1	21.88	GTG
PCG	nad4 (NADH dehydrogenase subunits IV)	7962	9287	-1	25.57	-
PCG	nad4l (NADH dehydrogenase subunits IV)	9281	9574	-1	23.47	-
tRNA	trnT (tRNA-Threonine)	9589	9654	1	21.21	TGT
tRNA	trnP (tRNA-Proline)	9655	9719	-1	27.69	TGG
PCG	nad6 (NADH dehydrogenase subunits VI)	9730	10212	1	25.05	-
PCG	cob (Cytochrome b)	10213	11349	1	34.39	-
tRNA	trnS2 (tRNA-Serine2)	11348	11413	1	22.73	TGA
PCG	nad1 (NADH dehydrogenase subunits I)	11421	12347	-1	29.34	-
tRNA	trnL1 (tRNA-Leucine1)	12348	12414	-1	19.4	TAG
rRNA	rrnL (rRNA-Large)	12413	13651	-1	23.08	-
tRNA	trnV (tRNA-Valine)	13650	13717	-1	25	TAC
rRNA	rrnS (rRNA-Small)	13717	14473	-1	22.85	-
	Control region	14474	16179	1	29.95	

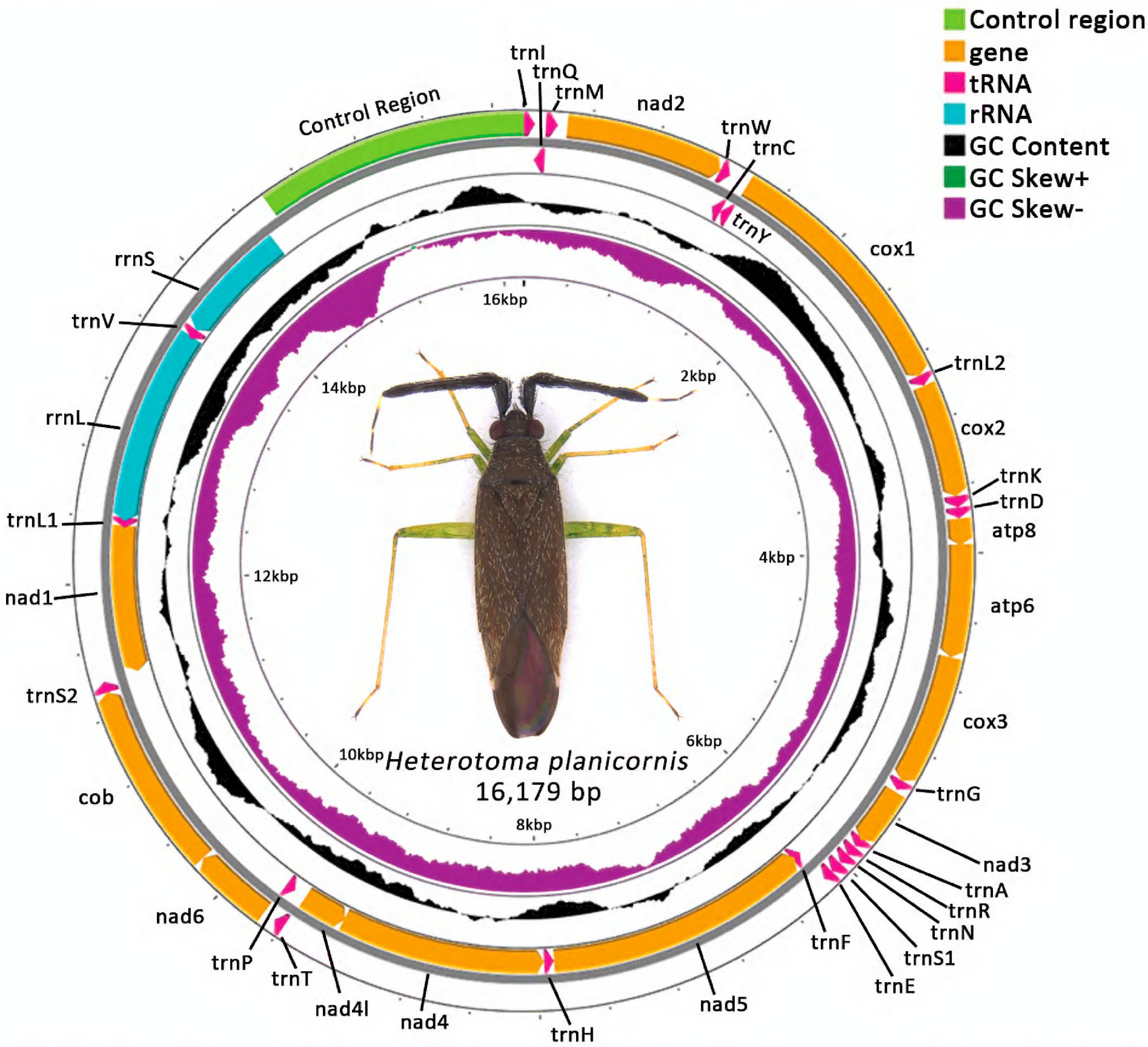

Figure 6. Mitochondrial genome of *Heterotoma planicornis*. Abbreviations of each gene were documented in Table 3. GC contents were indicated as a black circular graph, and GC-skew was indicated as green(+) or purple(-) in a circular graph. GC contents and GC skew were plotted as the deviation from the mean GC value of the full sequence. The innermost side of the circular graph shows sequence length, numerically marked with a 2 kbp interval. The circular map of the mitochondrial genome was visualized by the web server Proksee and annotated by MITOS2.

Table 4. Pairwise distances between analyzed *Heterotoma planicornis* specimens.

	***H. planicornis* HQ105735.1**	***H. planicornis* HQ105736.1**	***H. planicornis* Korea-Male-PV879916**	***H. planicornis* Korea-Male-PV789749**	***H. planicornis* Korea-5th_instar-PV850443**	***H. planicornis* Korea-Female-PV850444**
H. planicornis HQ105735.1						
H. planicornis HQ105736.1	0.0000					
H. planicornis Korea-Male- PV879916	0.0190	0.0198				
H. planicornis Korea-Male-PV789749	0.0000	0.0000	0.0180			
H. planicornis Korea-5th_instar-PV850443	0.0000	0.0000	0.0180	0.0000		
H. planicornis Korea-Female-PV850444	0.0190	0.0198	0.0000	0.0180	0.0180	

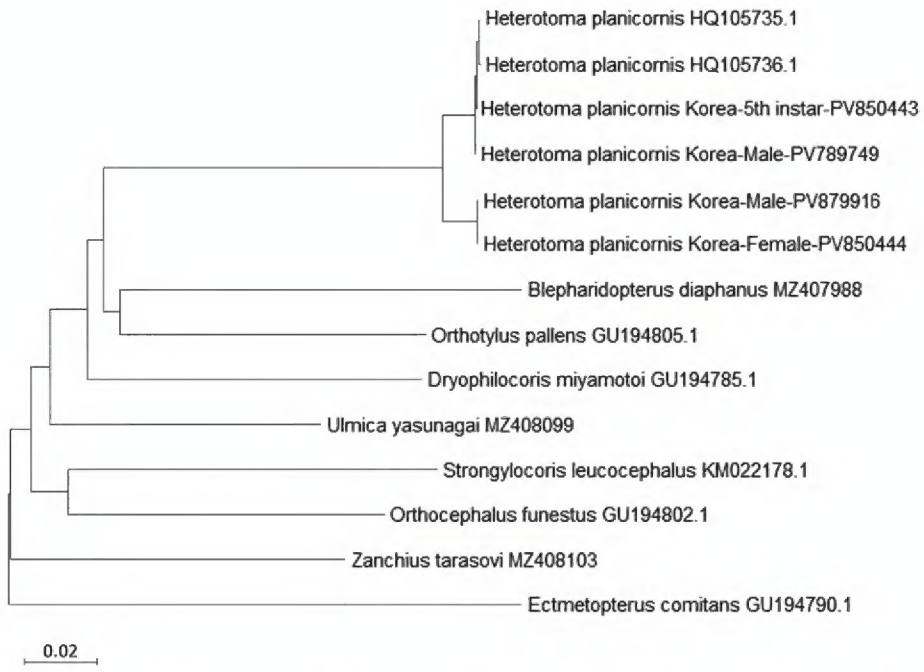

Figure 7. Neighbor-joining tree based on 14 COI sequences, including molecular data of Korean *Heterotoma planicornis*.

Discussion

Morphological features and anticipated introduction pathways of *H. planicornis* in Korea

Heterotoma planicornis is morphologically similar to *H. merioptera* (Scopoli, 1763), leading to considerable taxonomic confusion reviewed by Kment and Bryja (2006, 2012). Current diagnostic characters primarily rely on differences in genital structures and the length ratio of antennal segments II and III. *Heterotoma planicornis* tends to have a shorter second segment and a longer third segment compared to *H. merioptera* (Wagner 1968, 1974; Goula 1990). Additionally, Kment and Bryja (2006) proposed the ratio of vertex width to compound eye width as an alternative diagnostic character, but they noted that it overlaps between the two species.

The lengths of antennal segments III:II in the examined Korean specimens (0.289–0.303) were consistent with the value reported for *H. planicornis* by Kment and Bryja (2006). The presence of two apically sinuate, unfused endosomal sclerites and parameres in the examined specimens was consistent with the illustrations of *H. planicornis* provided by Tamanini (1962) and Goula (1990). However, a medially bifurcated sclerite, as in fig. 2 of Kment and Bryja (2012), was not observed in the Korean population. In the figures of the endosomal sclerites provided by Tamanini (1962), bifurcated sclerites were observed in both *Heterotoma* species. Considering that intraspecific variation in the branching of endosomal sclerites can occur in other species of Orthotylinae (Oh et al. 2022), the above differences are possibly due to variation. It is concluded that the Korean material examined pertains to *H. planicornis*.

Our study confirmed that the Korean *H. planicornis* uses *Spiraea japonica* as a breeding host. This plant species is native to Japan but has been widely planted in Europe since its introduction in the mid-19th century (Trees and Shrubs Online 2025). In Korea, cultivated *S. japonica* plants are mostly imported from Japan and European countries such as Germany and the Netherlands. Although various cultivars of *S. japonica* are cultivated in Japan, no species of the genus *Heterotoma* have been reported from the country or from any other locality in East Asia. Considering that all species of the genus *Heterotoma* are native to Europe, it is highly likely that individuals detected in Korea were introduced from populations in Europe, presumably on their host plants. Since eggs of *Heterotoma* species can overwinter and be transported with host saplings (Kment and Bryja 2006), the population might have been imported as eggs.

Molecular characteristics of Korean individuals of *Heterotoma planicornis*

Individuals used in the analysis were collected from the same plant, and no significant differences were observed in their external characteristics. An analysis of COI sequences from *H. planicornis* collected in this study and from taxonomically related species revealed that the Korean population comprises two distinct populations, exhibiting a 1.80–1.98% sequence difference (Table 4). This was also reflected in the NJ tree, where one population clustered with the North American population, while another branched into a separate node. However, due to the unavailability of European specimens, the relationship between Korean and European populations could not be ascertained. With sufficient sequence data on *H. planicornis* from diverse geographic regions, it could be possible to trace the origin and introduction pathway of the Korean population.

In species delimitation studies of Miridae using COI sequences, genetic distances less than 2% are largely considered conspecific (Jung and Lee 2012; Kim and Jung 2018). A recent DNA barcoding study by Kim and Jung (2018) on 273 individuals from 123 Miridae species revealed intraspecific variation ranging from 0 to 2.8%, with a mean variation of only 0.2%. Furthermore, in their analysis of 27 individuals from 14 Orthotylinae species, maximum intraspecific variation did not exceed 2%, while interspecific variation ranged from 1.6% to 27.5%. However, as currently only limited molecular data are available for populations of *H. planicornis*, further research is necessary.

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